

0590  
0411 #15

OIPF

## RAW SEQUENCE LISTING

DATE: 04/17/2003

PATENT APPLICATION: US/10/024,298A

TIME: 10:49:15

Input Set : A:\2003-04-07 1254-0191P.ST25.txt

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3 <110> APPLICANT: ASAHI KASEI KABUSHIKI KAISHA  
 4 Akio MATSUDA  
 5 Goichi HONDA  
 6 Shuji MURAMATSU  
 7 Yukiko NAGANO  
 9 <120> TITLE OF INVENTION: NF-K B Activating Gene  
 11 <130> FILE REFERENCE: 1254-0191P  
 13 <140> CURRENT APPLICATION NUMBER: 10/024,298A  
 C--> 14 <141> CURRENT FILING DATE: 2003-04-08  
 16 <150> PRIOR APPLICATION NUMBER: 60/314,385  
 17 <151> PRIOR FILING DATE: 2001-08-24  
 19 <150> PRIOR APPLICATION NUMBER: 60/278,641  
 20 <151> PRIOR FILING DATE: 2001-03-26  
 22 <150> PRIOR APPLICATION NUMBER: 60/258,315  
 23 <151> PRIOR FILING DATE: 2000-12-28  
 25 <150> PRIOR APPLICATION NUMBER: JP254018/2001  
 26 <151> PRIOR FILING DATE: 2001-08-24  
 28 <150> PRIOR APPLICATION NUMBER: JP0088912/2001  
 29 <151> PRIOR FILING DATE: 2001-03-26  
 31 <150> PRIOR APPLICATION NUMBER: JP402288/2000  
 32 <151> PRIOR FILING DATE: 2000-12-28  
 34 <160> NUMBER OF SEQ ID NOS: 182  
 36 <170> SOFTWARE: PatentIn Ver. 2.0  
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 48 20 25 30  
 50 Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser  
 51 35 40 45  
 53 Ala Gly Pro Pro Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln  
 54 50 55 60  
 56 Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly  
 57 65 70 75 80  
 59 Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly  
 60 85 90 95  
 62 Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr  
 63 100 105 110  
 65 Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro

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66          115          120          125
68 Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser
69          130          135          140
71 Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly
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74 Tyr Gly Gly Thr Arg Arg Arg
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85 <222> LOCATION: (194)..(694)
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90 ttcttgtggc ttggagtata atttagatta tacagaactt ggcctgcaga aactgaagga 120
92 gtctggaaag cagcacggct ttgcctcttt ctctgattat tattataagt ggtcctcggc 180
94 ggattcctgt aac atg agt gga ttg att acc atc gtg gta ctc ctt ggg 229
95          Met Ser Gly Leu Ile Thr Ile Val Val Leu Leu Gly
96          1          5          10
98 atc gcc ttt gta gtc tat aag ctg ttc ctg agt gac ggg cag tat tct 277
99 Ile Ala Phe Val Val Tyr Lys Leu Phe Leu Ser Asp Gly Gln Tyr Ser
100          15          20          25
102 cct cca ccg tac tct gag tat cct cca ttt tcc cac cgt tac cag aga 325
103 Pro Pro Pro Tyr Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg
104          30          35          40
106 ttc acc aac tca gca gga cct cct ccc cca ggc ttt aag tct gag ttc 373
107 Phe Thr Asn Ser Ala Gly Pro Pro Pro Pro Gly Phe Lys Ser Glu Phe
108 45          50          55          60
110 aca gga cca cag aat act ggc cat ggt gca act tct ggt ttt ggc agt 421
111 Thr Gly Pro Gln Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser
112          65          70          75
114 gct ttt aca gga caa caa gga tat gaa aat tca gga cca ggg ttc tgg 469
115 Ala Phe Thr Gly Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp
116          80          85          90
118 aca ggc ttg gga act ggt gga ata cta gga tat ttg ttt ggc agc aat 517
119 Thr Gly Leu Gly Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn
120          95          100          105
122 aga gcg gca aca ccc ttc tca gac tcg tgg tac tac ccg tcc tat cct 565
123 Arg Ala Ala Thr Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro
124          110          115          120
126 ccc tcc tac cct ggc acg tgg aat agg gct tac tca ccc ctt cat gga 613
127 Pro Ser Tyr Pro Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly
128 125          130          135          140
130 ggc tcg ggc agc tat tcg gta tgt tca aac tca gac acg aaa acc aga 661
131 Gly Ser Gly Ser Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg
132          145          150          155
134 act gca tca gga tat ggt ggt acc agg aga cga taaagtagaa agttggagtc 714

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135 Thr Ala Ser Gly Tyr Gly Gly Thr Arg Arg Arg
136          160          165
138 aaacactgga tgcagaaatt ttggattttt catcactttc tcttttagaaa aaaagtacta 774
140 cctgttaaca attgggaaaa ggggatattc aaaagttcgg tgggtgttatg tccagtgtag 834
142 ctttttgtat tctattattt gaggctaaaa gttgatgtgt gacaaaatac ttatgtgttg 894
144 tatgtcagtg taacatgcag atgtatattg cagtttttga aagtgatcat tactgtggaa 954
146 tgctaaaaat acattaattt ctaaaacctg tgatgcccta agaagcatta agaatgaagg 1014
148 tgttgtacta atagaaacta agtacagaaa atttcagttt taggtgggtg tagctgatga 1074
150 gttattacct catagagact gtaatatctt atttgggtatt atattatttg atgtttgctg 1134
152 ttcttcaaac atttaaatca agctttggac taattatgct aatttgtgag ttctgatcac 1194
154 ttttgagctc tgaagctttg aatcattcag tgggtggagat ggccttctgg taactgaata 1254
156 ttaccttctg taggaaaagg tggaaaataa gcatctagaa ggttgttgtg aatgactctg 1314
158 tgctggcaaa aatgcttgaa acctctatat ttctttcggt cataagaggt aaaggtcaaa 1374
160 tttttcaaca aaagtctttt aataacaaaa gcatgcagtt ctctgtgaaa tctcaaatat 1434
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166 <211> LENGTH: 339
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174 Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn
175   20          25          30
177 Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His
178   35          40          45
180 Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu
181   50          55          60
183 Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val
184   65          70          75          80
186 Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu
187   85          90          95
189 Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val
190   100         105         110
192 Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly
193   115         120         125
195 Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln
196   130         135         140
198 Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp
199  145         150         155         160
201 Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu
202   165         170         175
204 Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu
205   180         185         190
207 Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro
208   195         200         205
210 Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro
211   210         215         220
213 Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His

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214 225          230          235          240
216 Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr
217          245          250          255
219 Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile
220          260          265          270
222 Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp
223          275          280          285
225 Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn
226          290          295          300
228 Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys
229 305          310          315          320
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239 <211> LENGTH: 1924
240 <212> TYPE: DNA
241 <213> ORGANISM: Homo sapiens
243 <220> FEATURE:
244 <221> NAME/KEY: CDS
245 <222> LOCATION: (115)..(1131)
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250 cccagggttcg gcccgtaggc gtctggcagc ccggcgccat cttcatcgag cgcc atg 117
251 Met
252 1
254 gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc ggc 165
255 Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu Gly
256 5 10 15
258 ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc tgg aac gac 213
259 Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp
260 20 25 30
262 cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat 261
263 Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr
264 35 40 45
266 gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa 309
267 Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys
268 50 55 60 65
270 tgt gtt gga ggc aca gct ggt tgt gat tct tat acc cca aaa gtc ata 357
271 Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile
272 70 75 80
274 cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa tgt 405
275 Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys
276 85 90 95
278 aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg agc 453
279 Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser
280 100 105 110
282 tgt gaa ggc tat gag tcc tct gaa gac cag tat gta cta aga ggt tct 501
283 Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser

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284      115      120      125
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287 Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys
288 130      135      140      145
290 ctg aag gag tct gga aag cag cac ggc ttt gcc tct ttc tct gat tat 597
291 Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr
292      150      155      160
294 tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg att 645
295 Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile
296      165      170      175
298 acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc 693
299 Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe
300      180      185      190
302 ctg agt gac ggg cag tat tct cct cca ccg tac tct gag tat cct cca 741
303 Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro
304      195      200      205
306 ttt tcc cac cgt tac cag aga ttc acc aac tca gca gga cct cct ccc 789
307 Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro
308 210      215      220      225
310 cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggc cat ggt 837
311 Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly
312      230      235      240
314 gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa 885
315 Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu
316      245      250      255
318 aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta 933
319 Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile Leu
320      260      265      270
322 gga tat ttg ttt ggc agc aat aga gcg gca aca ccc ttc tca gac tcg 981
323 Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser
324      275      280      285
326 tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat agg 1029
327 Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg
328 290      295      300      305
330 gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca 1077
331 Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser
332      310      315      320
334 aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc agg 1125
335 Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg
336      325      330      335
338 aga cga taaagtagaa agttggagtc aaacactgga tgcagaaatt ttggattttt 1181
339 Arg Arg
341 catcactttc tcttttagaaa aaaagtacta cctgttaaca attgggaaaa ggggatattc 1241
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345 gttgatgtgt gacaaaatac ttatgtgttg tatgtcagtg taacatgcag atgtatattg 1361
347 cagtttttga aagtgatcat tactgtggaa tgctaaaaat acattaattt ctaaaacctg 1421
349 tgatgcccta agaagcatta agaatgaagg tgttgtacta atagaaacta agtacagaaa 1481
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## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/024,298A

DATE: 04/17/2003

TIME: 10:49:16

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